

FIGURE 1A

1 CGGGCCTGAGACTGGGGTGAUTGGGACCTAAGAGAACCTGAGCTGGAGGCCCGACAG
 61 CTGCTCTCGGGAGCCGCTCCCGACACCCGAGCCCCGCCGGCCTCCGCTCCGGCTC
 121 CCGGCTCCCTGGCTCCCTCGCCCTCCCCCGCCCTCGCCCGCCGAAGAGGGCCCCGGCT
 181 CCCGGGTGGAGCGCTGGGTCTGCCGGAAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT
 241 TCACTGAGCGATGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCAACCCCTTA

1 M G P E A L S S L L L L L L L
 301 GGCCCCAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTACTGCTGCTGCTCT

15 V A S G D A D M K G H F D P A K C R Y A
 361 TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTGATCCTGCCAAGTGCCGCTATG

35 L G M Q D R R T I P D S D I S A S S S W S
 421 CCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTGCTCCAGCTCCCTGGT

55 D S T A A R H S R L E S S D G D G A W C
 481 CAGATTCCACTGCCGCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGCCCTGGT

75 P A G S V F P K E E E Y L Q V D L Q R L
 541 GCCCCGCAGGGTCGGTGTCTCCCAAGGAGGAGGAGTACTTGCAAGGTGGATCTACAACGAC

95 H L V A L V G T Q G R H A G G G L G K E F
 601 TCCACCTGGTGGCTCGGTGGGACCCAGGGACGGCATGCCGGGGCTGGCAAGGAGT

115 S R S Y R L R Y S R D G R R W M G W K D
 661 TCTCCCGGAGCTACCGGCTGCGTTACTCCCGGATGGTCGCCGCTGGATGGCTGGAGG

135 R W G Q E V I S G N E D P E G V V L K D
 721 ACCGCTGGGTCAAGGAGGTGATCTCAGGCAATGAGGACCCCTGAGGGAGTGGTGCTGAAGG

155 L G P P M V A R L V R F Y P R A D R V M
 781 ACCTGGGCCCCCATGGTGGCCACTGGTGCCTTACCCCGGGCTGACCGGGTCA

175 S V C L R V E L Y G C L W R D G L L S Y
 841 TGAGTGTCTGCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTT

195 T A P V G Q T M Y L S E A V Y L I N D S T
 901 ACACCGCCCTGTGGGGAGACAAATGTATTATCTGAGGGCGTGTACCTCAACGACTCCA

215 Y D G H T V G G L Q Y G G L G Q L A D G
 961 CCTATGACGGACATAACCGTGGCGGACTGCAGTATGGGGCTGGCCAGCTGGCAGATG

235 V V G L D D F R K S Q E L R V W P G Y D
 1021 GTGTGGTGGGCTGGATGACTTAGGAAGAGTCAGGAGCTGCCAGGCTATGAGTTGAGT

255 Y V G W S N H S F S S G Y V E M E F E F
 1081 ACTATGTGGGATGGAGCAACCACAGCTTCCAGTGGCTATGTGGAGATGGAGTTGAGT

275 D R L R A F Q A M Q V H C N N M H T L G
 1141 TTGACCGGCTGAGGGCCCTCCAGGCTATGCAGGTCCACTGTAACAACTGACACAGCTGG

295 A R L P G G V E C R F R R G P A M A W E
 1201 GAGCCCGCTGCCCTGGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCTGGG

315 G E P M R H N L G G N L G D P R A R A V
 1261 AGGGGGAGCCCATGCCACAAACCTAGGGGCAACCTGGGGACCCAGAGCCCGGGCTG

335 S V P L G G R V A R F L Q C R F L F A G
 1321 TCTCAGTGCCCTTGGCGGCCGTGTGGCTCGCTCTGCAAGTGCCTCTCTTGCAG

355 P W L L F S E I S F I S D V V N N S S P
 1381 GGCCCTGGTACTCTCAGCAAATCTCCTCATCTGATGTGGTAACAATTCCCTCTC

FIGURE 1B

375 A L G G T F P P A P W W P P G P P P P T N
 1441 CGGCAGCTGGGAGGCACCTTCCGCCAGCCCCCTGGTGCCGCCCTGGCCACCTCCCACCA

395 F S S L E L E P R G Q Q P V A K A E G S
 1501 ACTTCAGCAGCTGGAGCTGGAGCCAGAGGCCAGCAGCCGTGGCCAAGGCCAGGGGA

415 P T A I L I G C L V A I I L L L L I I
 1561 GCCCGACCGCCATCCTCATCGGCTGGCTGGCCATCATCCTGCTCCTGCTGCTCATCA

435 A L M L W R L H W R R L L S K A E R R V
 1621 TTGCCCTCATGCTCTGGCGCTGCACTGGCGAGGCTCCTCAGCAAGGCTAACGGAGGG

455 L E E E L T V H L S V P G D T I L I N N
 1681 TGTTGGAAGAGGAGCTGACGGTTACCTCTGTGCCCCAGGGACACTATCCTCATCAACA

475 R P G P R E P P P Y Q E P R P R G N P P
 1741 ACCGCCAGGTCCCTAGAGAGCCACCCCCGTACAGGAGCCCCGGCCTCGTGGAAATCCGC

495 H S A P C V P N G S A L L L S N P A Y R
 1801 CCCACTCCGCTCCCTGTGCCCCAATGGCTCTGCGTTGCTCTCCAATCCAGCCTACC

515 L L L A T Y A R P P R G P G P P T P A W
 1861 GCCTCCTCTGGCCACTTACGCCGTCCTCGAGGCCGGGGCCCCCACACCCGCCT

535 A K P T N T Q A Y S G D Y M E P E K P G
 1921 GGGCAAACCCACCAACACCCAGGCCTACAGTGGGACTATATGGAGCCTGAGAAGCCAG

555 A P L L P P P P Q N S V P H Y A E A D I
 1981 GCGCCCCGCTCTGCCACCTCCCCAGAACAGCGTCCCCATTATGCCAGGGCTGACA

575 V T L Q G V T G G N T Y A V P A L P P G
 2041 TGTTACCCCTGCAGGGCGTCACCGGGGCAACACCTATGCTGTGCGCTGCACTGCCAGG

595 A V G D G P P R V D F P R S R L R F K E
 2101 GGGCAGTCGGGGATGGCCCCCAGAGTGGATTCCCTCGATCTCGACTCCGCTCAAGG

615 K * L G E G Q F G E V H L C E V D S P Q D
 2161 AGAAGCTGGCGAGGGCCAGTTGGGAGGTGCACCTGTGAGGTGACAGCCCTCAAG

635 L V S L D F P L N V R K G H P L L V A V
 2221 ATCTGGTCAGTCCTGATTTCCCCCTTAATGTGCGTAAGGGACACCTTGTGGTAGCTG

655 K I L R P D A T K N A S F S L F S R N D
 2281 TCAAGATCTACGCCAGATGCCACCAAGAACATGCCAGCTCTCTCCAGGAATG

675 F L K E V K I M S R L K D P N I I R L L
 2341 ATTCCCTGAAAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCACATCATCGGCTGC

695 G V C V Q D D P L C M I T D Y M E N G D
 2401 TGGCGCTGTGTGCGAGGACGCCCTCTGCATGATTACTGACTACATGGAGAACGGCG

715 L N Q F L S A H Q L E D K A A E G A P G
 2461 ACCTCAACCAGTCCTCAGTGGCCACCAAGCTGGAGGACAAGGCAGCCAGGGGGCCCTG

735 D G Q A A Q G P T I S Y P M L L H V A A
 2521 GGGACGGGCAGGCTGCCAGGGCCACCATCAGCTACCCAAATGCTGCTGACATGGCAG

755 Q I A S G M R Y L A T L N F V H R D L A
 2581 CCCAGATCGCCTCCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATGGACCTGG

775 T R N C L V G E N F T I K I A D F G M S
 2641 CCACGCGGAACCTGCCTAGTTGGGAAAATTCACCATCAAAATCGCAGACTTTGGCATGA

FIGURE 1C

795 R N L Y A G D Y Y R V Q G R A V L P I R
 2701 CCCGGAACCTCTATGCTGGGACTATTACCGTGTGCAGGGCCGGGAGTGCTGCCCATCC
 815 W M A W E C I L M G K F T T A S D V W A
 2761 GCTGGATGCCCTGGGAGTGCATCCTCATGGGAAGTCACGACTGCGAGTGACGTGTGGG
 835 F G V T L W E V L M L C R A Q P F G Q L
 2821 CCTTTGGTGTGACCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTGGGCAGC
 855 T D E Q V I E N A G E F F R D Q G R Q V
 2881 TCACCGACGAGCAGGTATCGAGAACGCGGGGAGTTCTCCGGGACCAGGGCCGGCAGG
 875 Y L S R P P A C P O G L Y E L M L R C W
 2941 TGTACCTGTCCCCGGCCGCTGCCCCAGGGCTATATGAGCTGATGCTTCGGTGCT
 895 S R E S E Q R P P F S Q L H R F L A E D
 3001 GGAGCCGGGAGTCGAGCAGCACCACCTTCCAGCTGCATCGGTTCCCTGGCAGAGG
 915 A L N T V
 3061 ATGCACTAACACGGTGTGAATCACACATCCAGCTGCCCTCCCTCAGGGAGTGATCCAG
 3121 GGGAAAGCCAGTGCACACTAAAACAAGAGGACACAATGGCACCTCTGCCCTCCCTCCGA
 3181 CAGCCCCATCACCTCTAATAGAGGGCAGTGAGACTGCAGGTGGCTGGGCCACCCAGGGAG
 3241 CTGATGCCCTTCTCCCTCTGAGACACACTCTCATGCCCCCTCTGTTCTCCCTCC
 3301 TAGAAGCCCCCTGTCGCCCCACCCAGCTGGTCTGTGGATGGATCCCTCTCCACCCCTCC
 3361 AGCCATCCCTGGGGAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGGCCATTG
 3421 GAGCAGCTGGGCCCACTGGACAAACACTGATCCGGAGAGGTGGCTGCGCCTCAGCTTC
 3481 TCTCTCCCTGTACACACTGGACCCCACTGGCTGAGAATCTGGGGTGAGGAGGACAAGA
 3541 AGGAGAGGAAAATGTTCTGTGGCTGCTCTGTAATGTCCTCAGCTGGCTCTTC
 3601 CTCCCTCCATCACCTGAAACACTGGACCTGGGGTAGGCCCGCCCCAGCCCTCAGTCACCC
 3661 CCACTTCCCACTGCACTGCTGAGCTAGAACCTCTCTAAGCCTATAACGTTTCTGTGGAG
 3721 TAAATATTGGGATTGGGGAAAGAGGGAGCAACGGCCCATAGCCTGGGTTGGACATC
 3781 TCTAGTGTAGCTGCCACATTGATTTCATAATCACTTGGGTTGTACATTGGGG
 3841 GGAGAGACACAGATTTTACACTATATATGGACCTAGCTTGAGGAATTAAATCCCT
 3901 GCACTAGGCAGGTAAATAAAGGTTGAGTTCCACAAAAAAACCGGAAT
 3961 TC

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FIGURE 2

MCK-10 Splice Variants

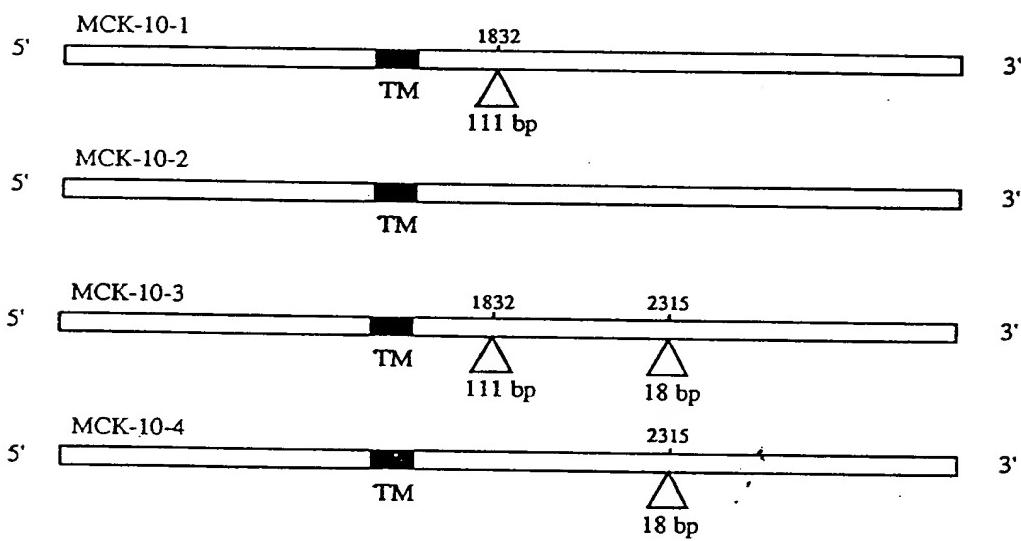


FIGURE 3A

FIGURE 3B

D K Q V L O G N S N P Y D I F L K D L E P -
 cccattgttagccagattgtccggtcatccaggcaccactccatgaatgttgt
 842 gggtaacatcggtctaaacccggcaagaatggcgtggctgggtgaggcttacacaca 901

b P I V A R F V R F I P V T D H S M N V C -
 atgagagtgtaggtttacggCTGTGTCGGCTAGATGGCTGGYGTCTAACATGCTCA
 902 tacatccatcgaeatgccGACACAGACCAGTCAACCGAACACAGAAATGTTACGAGGT 961

b M R V E L Y G C V H L O G L V S Y H A P -
 GCTGGGGCAGCAGTTGTACTCCCTGGAGGTCCATCATTTATCTGAATGATTCTGTCTAT
 962 CGACCCGTCGTCACACATGAGGGACCTCCAAGGTAGTAAATAGACTTAAGACAGATA 1021

b A G Q Q F V L P G G S I I Y L H D S V Y -
 GATGGAGCTGTTGGATACAGCATGACAGAAGGGCTAGGCCATTGACCCATGGTGTCT
 1022 CTACCTCGACAACCTATGTCGTACTGTCCTCCGATCCGGTTACTGGCTACCACACAGA 1081

b D G A V G Y S H T E G L G Q L T D G V S -
 GCCCTGGACGATTTCACCCAGACCCATGAATAACACAGTGTGGCCGGCTATGACTATGTG
 1082 CCGGACCTGCTAAAGTGGGTCTGGTACTTATGGTGCACACCGGGCCGATACTGATAACAC 1141

b G L O D F T Q T H E Y H V W P G Y D Y V -
 GGCTGGGGAAACGAGAGTGGCACCAATGGCTACATTGAGATCATGTTGAATTGGACCGC
 1142 CCGACCGCCTTGCTCTCACGGTGGTACCGATGTAACTCTAGTACAACACTAAACTGGCG 1201

b G W R N E S A T H G Y I E I M F E F D R -
 ATCAGGAATTTCACTACCATGAAGGTOCACTGCAACAACATGTTGCTAAAGGTGTGAAG
 1202 TAGTCTTAAAGTGTGGTACTTCCAGGTGACGTGTTGACAAACGATTCCACACTTC 1261

b I R H F T T H K V H C R N N H F A K G V K -
 ATCTTAAAGGAGGTACAGTGTACTTCGGCTCTGAAGGCCAGTGAGTGGTACCTAATGCC
 1262 TAGAAATTCTCCATGTCAGATGAAGGGGAGACTTCGGTCACTCACCCATGGATTACGG 1321

b I F K E V Q C Y F R S E A S E H V P H A -
 ATTTCCCTTcccccttgcctggatgacgtcaacccaggctcggtttgtcacggtgect
 1322 TAAAGGAAggggaaacaggacactgtcgatgtgggtcacgacccaaacgtctatggattacgg 1381

b I S F P L V L D D V H P S A R F V T V P -
 ctccaccaccgaatggccaggccatcaatggccatcgatgtcaataccatggccatggat
 1382 gaggtggcttacccgtcacggtagttacgttatgttacaaacgtctatggattac 1441

b L H H R M A S A I K C Q Y H F A D T W H -
 atgttcagttagatcacctccaatcgatgtcaatgtacaacaactctgaagccctg
 1442 tacaatgtactctatgttacggatgttacgttacatgttgcacttgcggac 1501

b M F S E I T F Q S D A A M Y H N S E A L -
 cccaccccttccatggcaccaccaacccatgtccatgtttaatccctccatggccatggat
 1502 ggggtggagaggataccgtgggtgtggatactaggatgttacgttacactgtcg 1561

b P T S P M A P T T Y D P M L K V D O S H -
 actcgatccatgtggctgtggccatcatcttccatggccatggat
 1562 tgccctaggactaacccgaccaaccaccggtagtagaaataggaggaccggtagtaacag 1621

b T R I L I G C L V A I I F I L L A I V -
 atcattccatggaggcagtctggcagaaaatgtggagaaggcttctcgaggatgtg
 1622 tagtagggacccgtcaagaccgtctttacccatccgttccggaaagacgtcciacac 1681

b I I L H R Q F H Q K M L E K A S R R H L -
 gatgtgaaatgacagtcagecttccctgccaagtgatcgatgttcaacaataac

FIGURE 3C

1682 ctactactttactgtcagtccggaaaggccgggtcacatcaagatcgatcaaggatgttatttg 1741
 b D D E M T V S L S L P S D S S M F K N N -
 cgctccctcatcaccttagtgzacaagggtccacactcgacttacgatcgatcttccccctt
 1742 gcgaggagtatggatcaccttgttccacggttgagctgatcgatcgatagaaggaa 1801
 b R S S S P S E Q G S M S T Y O R I F P L -
 cgccctgactacCAGGAGCCATCCAGGCTGATACGAAAACCTCCAGAATTTCCTCCAGGG
 1802 gcgggactgatgTCCTCGGTAGGTCCGACTATGCTTTGAGGGTCTAACGAGGTCCC 1861
 b R P D Y Q E P S R L I R K L P E F A P G -
 GAGGAGGAGTCAGGCTGCAGCGGTGTTGTGAAGCCAGTCCAGGCCAGTGGCCCTGAGGGG
 1862 CTCCTCCCTCAGTCCGACGTCGCCACAACACTTCGGTCAGGTCCGGTCAACGGGACTCCCC 1921
 b E E E S G C S G V V K P V Q P S G P E G -
 GTGGCCCACTATGCAGAGGCTGACATAGTGAACCTCCAAGGAGTGACAGGAGGAACACA
 1922 CACGGGGTGTACGTCCTCGACTGTATCACTTGGAGGTCTCTCACTGTCTCCGTGTG 1981
 b V P H Y A E A D I V N L Q G V T G G N T -
 TACTCAGTGCCTGCCGTCAACCATGGACCTGCTTCAGGAAAAGATGTGGCTGTGGAGGAG
 1982 ATGAGTCACCGACGGCAGTGGTACCTGGACGAGAGTCCTTCTACACCGACACCTCTC 2041
 b Y S V P A V T H O L L S G K D V A V E E -
 TTCCCCAGGAAACTCTTAACCTTCAAAGAGAAGCTGGAGAAGGACAGTTGGGGAGGTT
 2042 AAGGGGTCTTIGAGGATTGAAAGTTCTCTCGACCTCTCTCTCAAAACCCCTCAA 2101
 b F P R K L L T F K E K L G E G Q F G E V -
 CATCTCTGTGAAGTGGAGGGAAATGGAAAAAATCTAAAGACAAAGATTTGCCCTAGATGTC
 2102 GTAAQAGACACTTCACCTCCCTTACCTTTAAAGTTCTGTCTCTAAACGGGATCTACAG 2161
 b H L C E V E G M E K F K O K D F A L O V -
 AGTGCCAACAGCCTGCTCTGGCTGTGAAATGCTCCGAGCAGATECCAACAGAAAT
 2162 TCACGGTTGGTCGGACAGGACCACGACACTTCACGAGGCTGCTACGGTTGTTCTTA 2221
 b S A N Q P V L V A V K H L R A D A N K N -
 GCCAGGAATGATTTCTTAAGGAGATAAAGATCATGTCCTGGCTCAAGGACCCAAACATC
 2222 CGGTCTTACTAAAGAATTCTCTATTCTAGTACAGAGCCGAGTTCTGGGTTGTAG 2281
 b A R K O F L K E I K I H S R L K D P N I -
 ATCCATCTATTAGCTGTGTATCACTGATGACCCCTCTGTATGATCACTGAATACTG
 2282 TAGGTAGATAATGACACACATAGTGACTACTGGGAGAGACATACTAGTCACTTATGTAC 2341
 b I H L L A V C I T D D P L C H I T E Y H -
 GAGAAATGGAGATCTCAATCAGTTCTTCCCGCCACGAGCCCCCTAAATCTCTCCAGC
 2342 CTCTTACCTCTAGAGTTAGTCAAAGAAAGGGCGGTGCTGGGGgATTAAGAAGGAGGTG 2401
 b E R G O L N Q F L S R H E P P N S S S S -
 GATGTACCCACTGTCAGTTACACCAATCTGAAGTTATGGCTACCCAAATTGCCCTGGC
 2402 CTACATGGTGAAGTCATGTGGTAGACTTCAAATACCGATGGTTAACGGAGACCG 2461
 b O V R T V S Y T N L K F M A T Q I A S G -
 ATGAAGTACCTTCTCTTAATTGGTCAACCGAGATCTGGCCACACGAAAATGTGTTA
 2462 TACTTCATGGAAAGGAGAGATAAAACATGTGGCTCTAGACCGGTGTTGACAAAT 2521
 b H K Y L S S L N F V H R D L A T R N C L -
 GTGGGTAAAGAAACTACACAACTCAAGATAGTGACTTTGGATGAGCAGGAACCTGTACAGT
 2522 CACCCATTCTGATGTGTTAGTTCTATCGACTGAAACCTTACTCGTCCTGGACATGTCA 2581
 b V G K N Y T I K I A D F G H S R H L Y S -

FIGURE 3D

2582 GGTGACTATTACCGGATCCAGGGCGGGCAGTGCTCCCTATCCGCTGGATGTCTGGAG
 CCACTGATAATGCCCTAGGTCCCGGCCGTACGAGGGATAGGCACCTACAGAACCCCTC 2641
 b G D Y Y R I Q G R A V L P I R H M S K E -
 2642 AGTATCTGCTGGGCAAGTTCACTACACCAAGTGATGTGTCGGGCTTTGGGTTACTTTG
 TCATAGAAACGACCGTTCAAGTGATGTGCGTTCACTACACACCCGGAAACCCCAATGAAAC 2701
 b S I L L G K F T T A S O V H A F G V T L -
 2702 TGGGAGACTTCACCTTTGCAAGAACAGCCCTATTCCAGCTGTCAAGATGAACAGGTT
 ACCCTGAAAGTGGAAACAGTTCTTGTCGGGATAAGGGTCGACAGTCTACTTGTCAA 2761
 b H E T F T F C Q E Q P Y S Q L S D E Q V -
 2762 ATTGAGAATACTGGAGAGTTCTCCGAGACCAAGGGAGGCAGACTTACCTCCCTCAACCA
 TAATCTTATGACCTCTCAAGAAGGCTCTGGTTCCTCCGCTGAATGGAGGGAGTTGGT 2821
 b I E R T G E F F R D Q G R Q T Y L P Q P -
 2822 GCCATTTGCTCTGACTCTGTATAAGTGATGCTCAGCTGCTGGAGAAGAGATACGAAG
 CGGTAAACAGGACTGAGACACATATTGACTAGTGAGTCGAGGAACCTTCTCTATGCTTC 2881
 b A I C P D S V Y K L M L S C H R R O T K -
 2882 AACCGTCCCTCATCCAAGAAATCCACCTCTGCTCTTCAACAAGGCCACGGAGTGATGC
 TTGGCAGGGAGTAAGGTTTTAGGTGGAAGACGAGGAAGTTGTCGGCTGCTCACTAGG 2941
 b K R P S F Q E I H L L L L Q Q G D E -
 2942 TGTCACTGCTGGCATGTTCTACGGCTCAGGTCTCCCTACAAGAACCTACACTCACCC
 ACAGTCACGGACCGGTACAAGGATGCCAGTCCAGGAGGGATGTTCTGGATGGTGAGTG 3001
 b
 3002 CATGCCTATGCCACTCCATCTGGACATTAAATGAAACTGAGAGACAGAGGGCTGGTTGCT
 GTACGGATAACGGTAGGGTAAATTACTTGTACTCTCTGCTCCGAACAAACGA 3061
 b
 3062 TTGCCCCCTTTCTGGTACCCCCACTCCCTACCCCTGACTCATATATACTTTTTTT
 AACGGGAGAAAAGGACCACTGGGGTGAGGGATGGGGACTGAGTATATGAAAAAAA 3121
 b
 3122 TTACATTAAGAACTAAAAAAAAAAAAAGGCG 3158
 AATGTAATTTCTGATTTTTTTTTTTTTCCGC
 b

FIGURE 4A

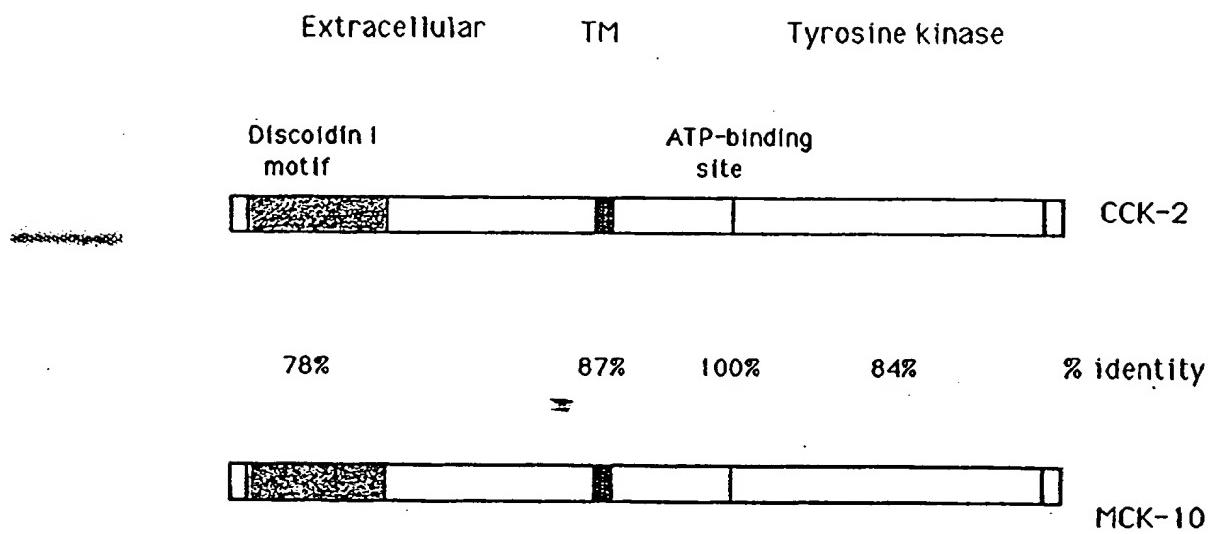
ATP-binding site

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1 ..MGPEALSSLLLLLVLASGQADMKGHFDPAKCRYALGHQDRTIPDSOIS	48	MCK-10
48 ASSQHSESTAAKYGRLDSEEGDGAHCPEIPVPEPOOLKEFLQIDLHTLHF	97	
49 ASSSHSOSTAARHSRLESSOGDGAHCAGSVFPKE.EEYLQVOLQLHLV	97	
98 TLVGTQGRRAAGGGIEFAPHYKINYSRDGTRWISHWRNRHKGKVLGDGSNP	147	
98 ALVGTQGRRIAGGLKEFSRSYRLRYSROGRRHMGKDRWQEVISGHEDP	147	
148 YDIFLKDLEPPPIVARFVRFIPVTDHSMNVCHRVELYGCVMVLDGLVSYKAP	197	
148 EGWLKDGLGPPMVAVLVRFIPRADRVMSVCLRVELYGLKLRDGLLSYTAP	197	
198 AGQQFVLPGGSIIYTLDNSVYDG.AVGYSKTEGLGQLTDGVSGLDDFTQTH	246	
198 VGGTMYLSEA..VYLNOSTYDGHTVGGLQYGGLGQLADGVWGLDDFRKSQ	245	
247 EYHVKPGYDYYGVGRNESATNGYEIEMEFDFIRNFTTMKVHCNNHFAKGV	296	
246 ELRVKPGYDYYGVGSNSHFSSGYVEMEFDFORLRAFQAMQVHCNNHHTLGA	295	
297 KIFKEVQC.YFRSEASEWVVPNAISFPLVLDVNPSARFVTVPVHLHRKASA	345	
296 RLPGGVCECRFRGPAAKEGEPMRHNLLGGNLGDPRARAVSVPLGGRVAF	345	
346 IKCQYHFADTYMKHFEITFQSOAAMYNHSÉALPTS.....	380	
346 LQRFLFLAGPMLLFLSEISFISO.VVHNSSPALGGTFPPAPKPPGPPPTN	394	
381PKAPTTYDPMLKVDOOSNTRILIGCLVAJIFILLAIIVIILWKRQFWQ	426	
395 FSSLELEPRQQPVAKAEGSPTAILIGCLVAJILLIILALMLKRLKMR	444	
427 KMELEKASRRMIDDEMTVSLSLPSDSSMFNNNNRSSSPSEQSKSTYDRIFF	476	
445 RLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREG.....	481	
477 LRPOYQEPSRLIRKLPEFAPGEEESGCSG.....VVKPVQPSGPEGV	518	
482 ..PPYQEPRPRGNPPHSAPCVPHGSATSGDYHEPEKPGAPLPPPPQNSV	527	
519 PHYAEADIVA...VGGHTYVPAVTMDLISGKOVAVEEFPRKLLTFKEK	560	
530 PHYAEADIVTLQGVGGNTYAVPALPPGAVGDGPPRV.OFPRSLRFKEK	578	
569 LGEGQFGEVHLCEVEGHEKFKKDKOFALDVSANQPVLVAVKHLRADANKA	618	
579 LGEGQFGEVHLCEVDPQOLVSLDFPLNKVRKGHPLLVAVKILRPDTAKNA	628	
619 RNDFLKEIKIMSRLKOPNIHLLAVCITODPLCHÍTEYHÉNGDLHQFLSR	668	
629 RNDFLKEVKIMSRLKOPNIIRLLGVCVQDOPLCMIDYHENGDLHQFLSA	678	
669 HE.....PPNSSSSDVRTVSYTNLKFMATQIASGMKYLSSLKFVHR	709	
679 HQLEDKAAEGAPGDGQAAGGPTISYPHLLLHVAAQIASGMRYLATLNFVHR	728	
710 DLATRNCLVGKHTIKIAADFQMSRNLYSGOYRJQGRAVLPIRKHSKESI	759	
729 DLATRNCLVGENFTIKIAADFQMSRNLYAGDGYRVQGRAVLPIRKHSKESI	778	
760 LLGKFTTASDVHAFGVTLMETFTFCQEQPYSQSLSDEQVIENTGEFFRQDG	809	
779 LMHKFTTASDVHAFGVTLMEVLMHLCRAQPFQQLTDEQVIEAGEFFRQDG	828	
810 RQTYLPQPAICPDPSVYKLHLSCHRRDTKRNPSFQEIHLLLQQGDE..	855	
829 RQVYLSRPPACPQGLYELMLRCWSRESEQRPPFSQLNRAEDALNTV	876	

Transmembrane region

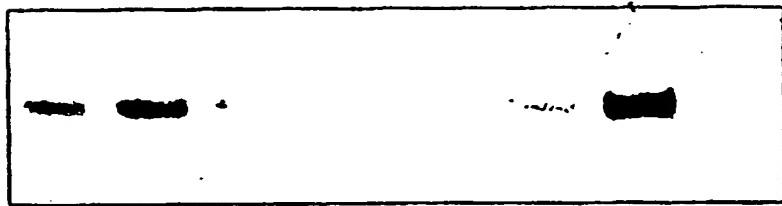
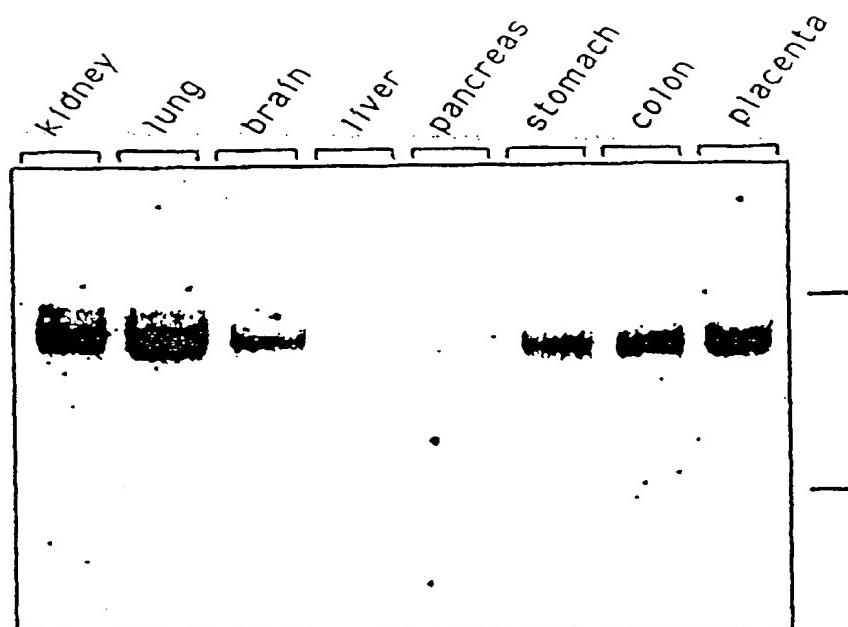
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Figure 4B



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FIGURE 5A



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FIGURE 5B

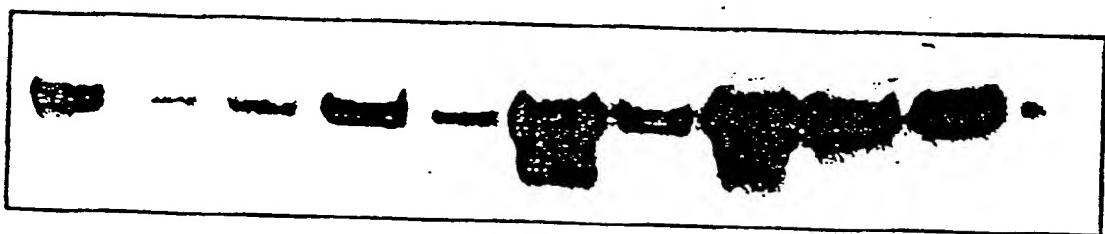
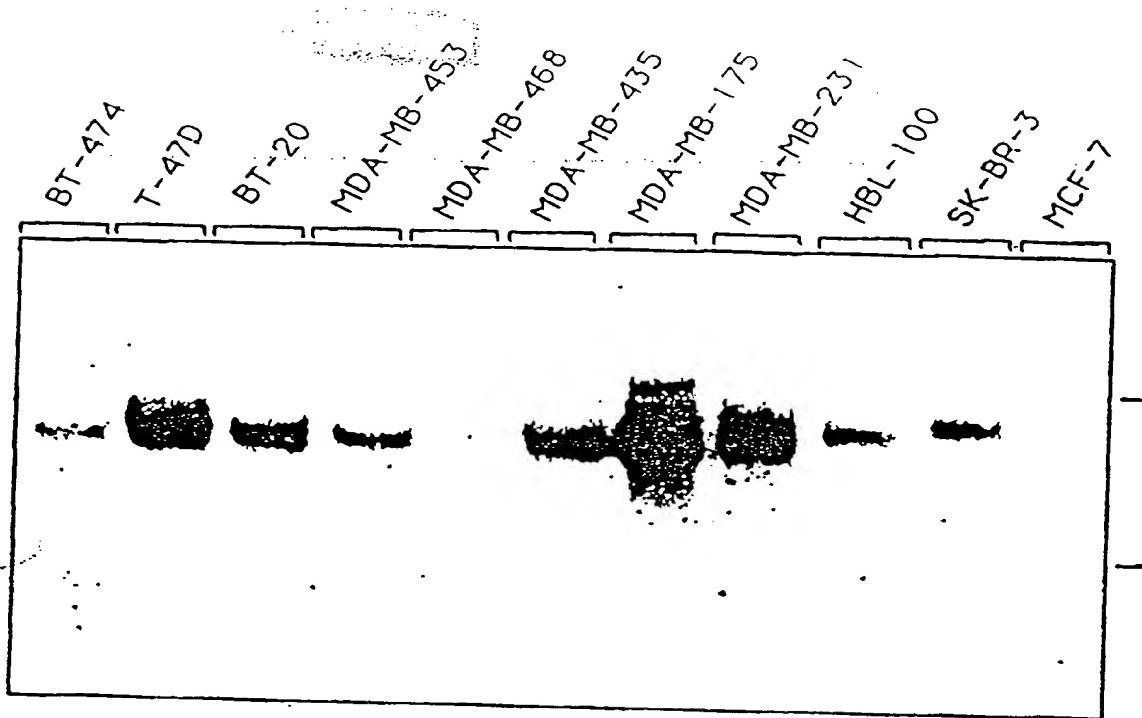


FIGURE 5C

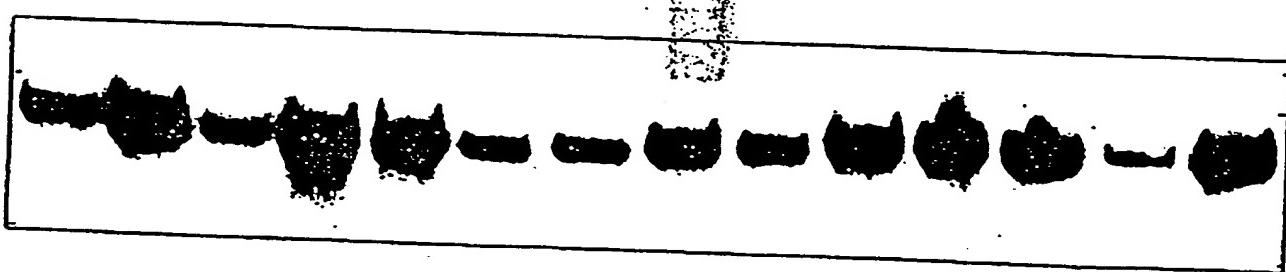
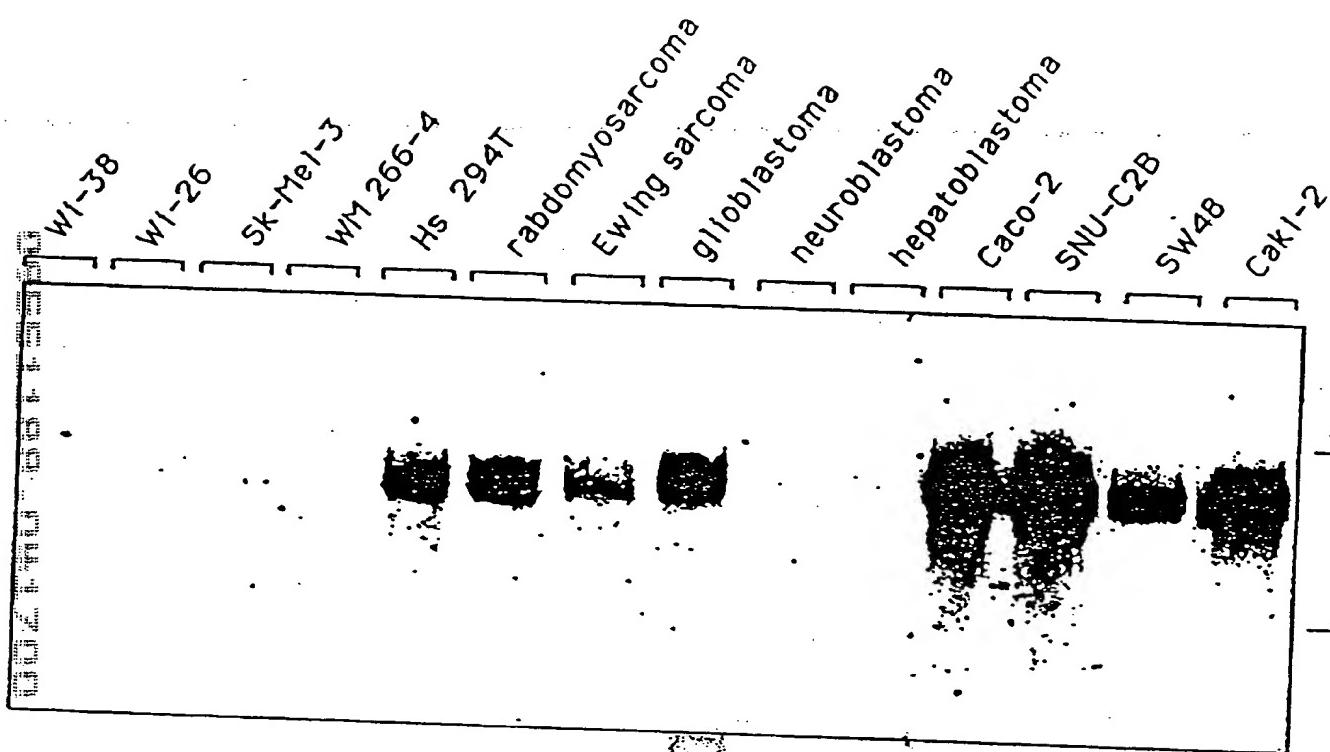
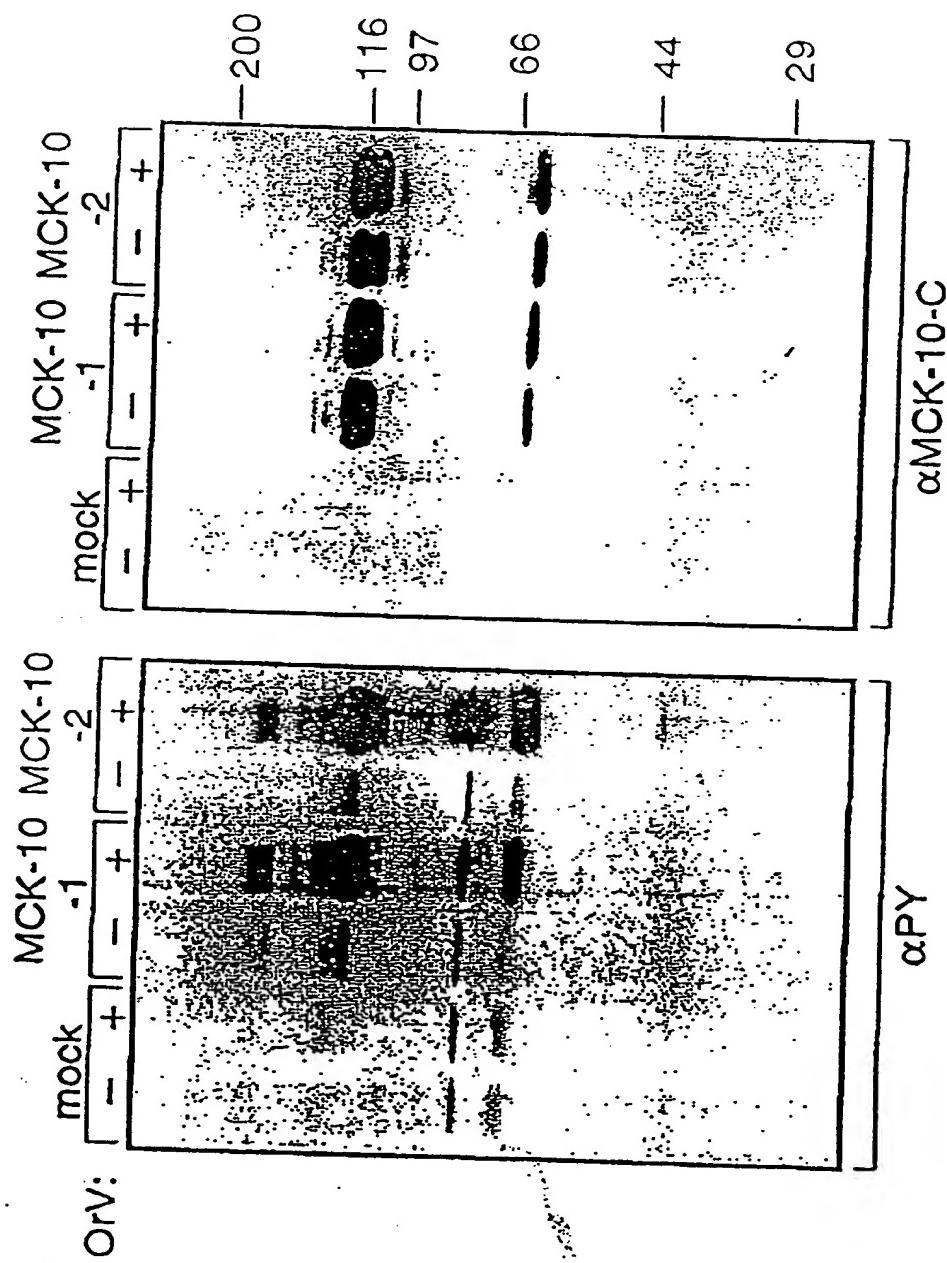


FIGURE 6A



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FIGURE 6B

Tu.

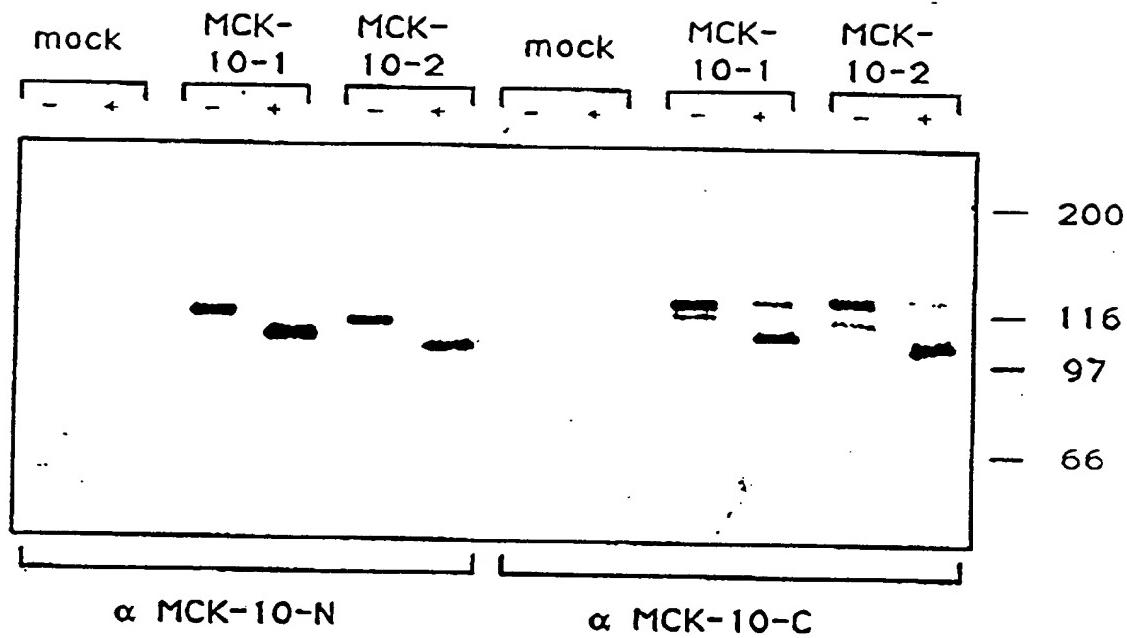
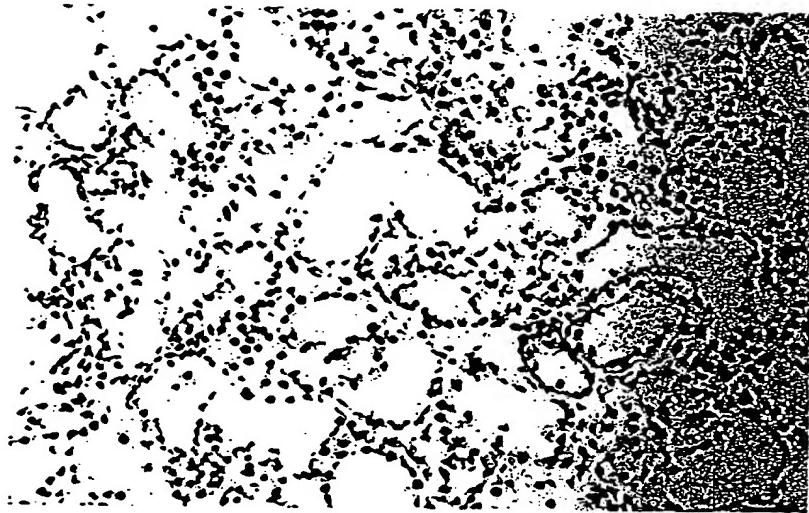


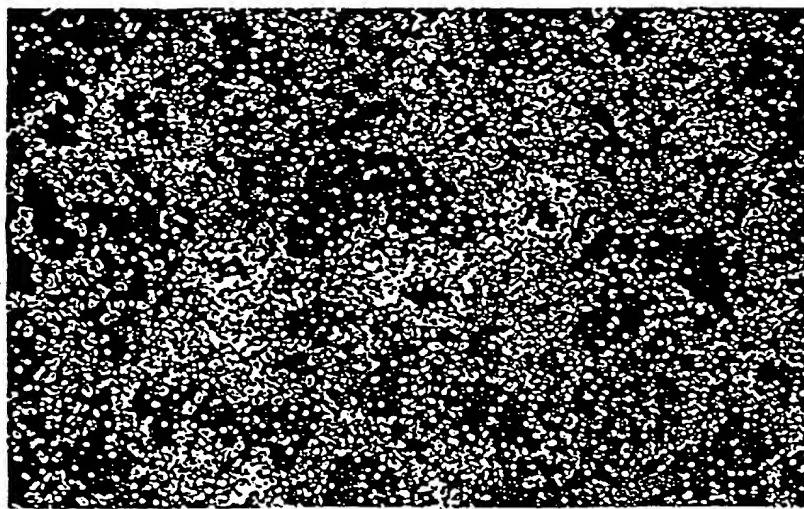
FIGURE 7A

lightfield



darkfield

FIGURE 7B

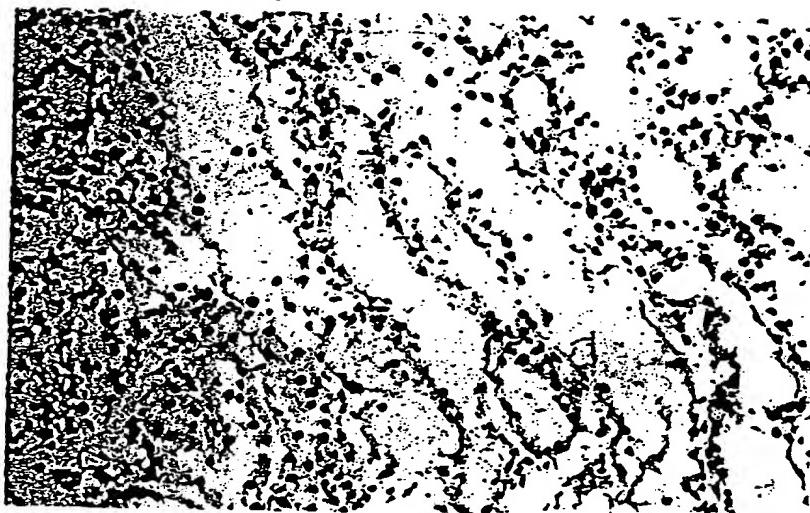


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FIGURE 8A

lightfield



darkfield

FIGURE 8B

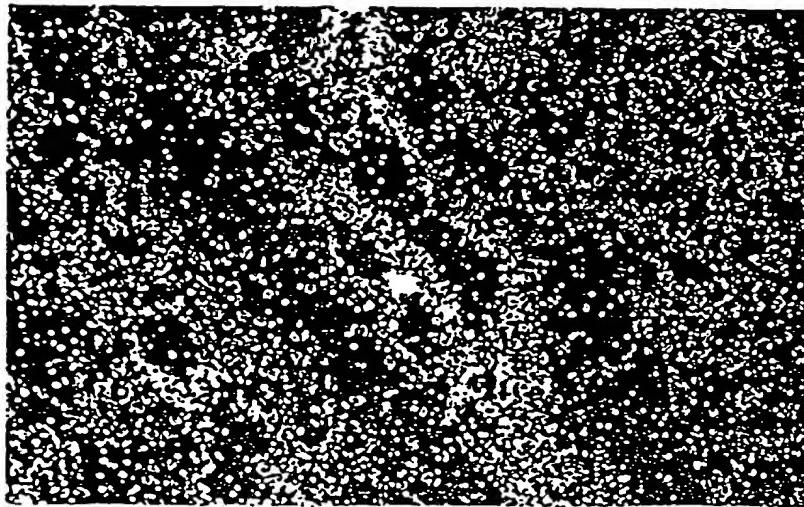
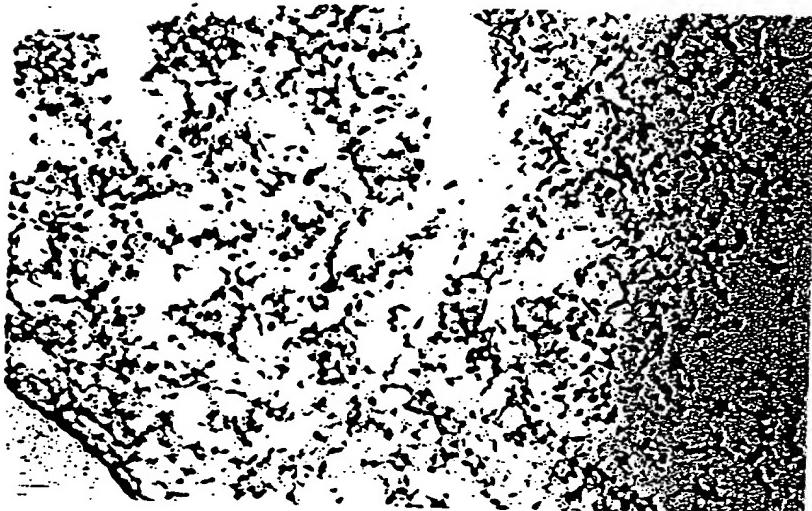


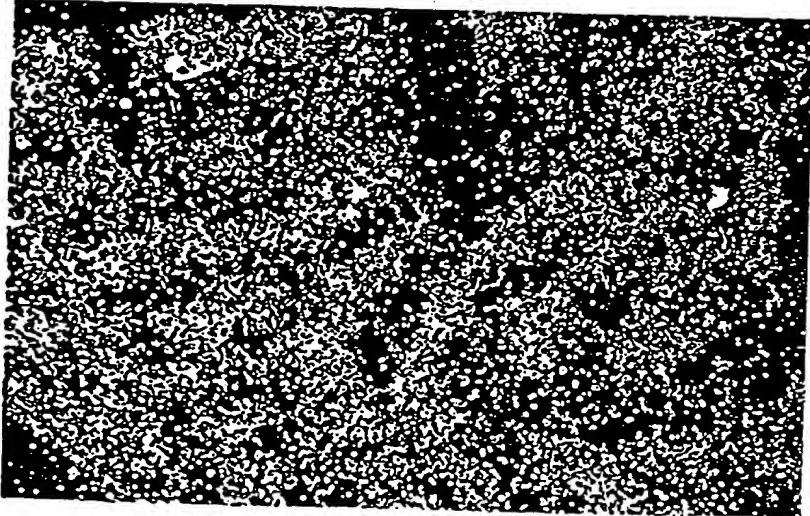
FIGURE 9A

lightfield



darkfield

FIGURE 9B



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FIGURE 10A

lightfield



darkfield

FIGURE 10B

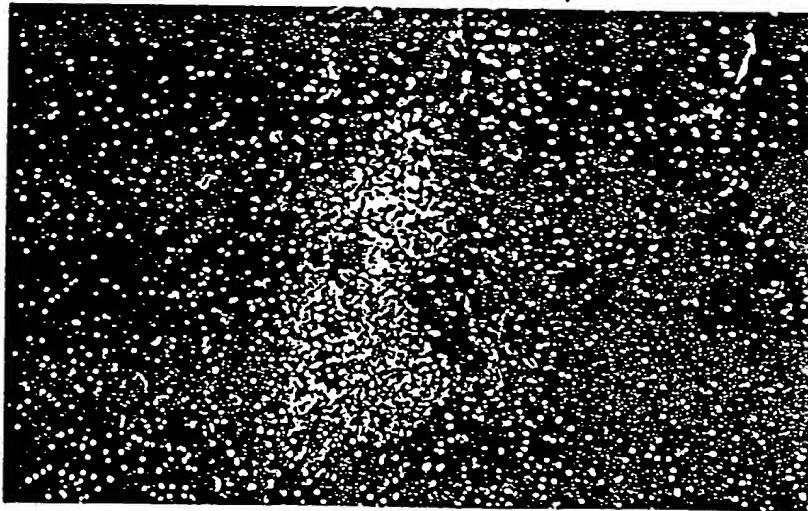
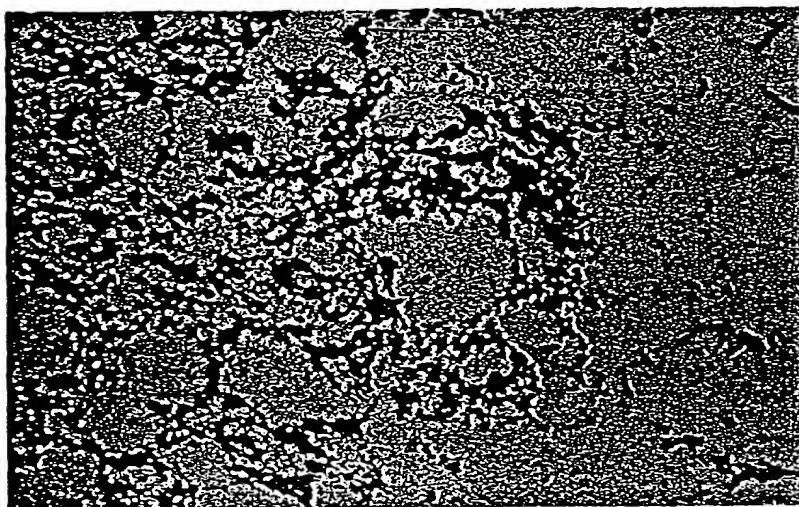


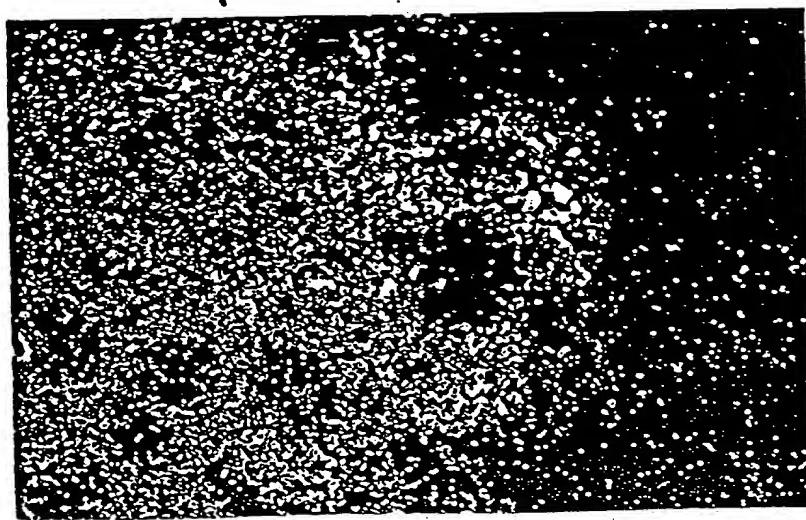
FIGURE II A

lightfield



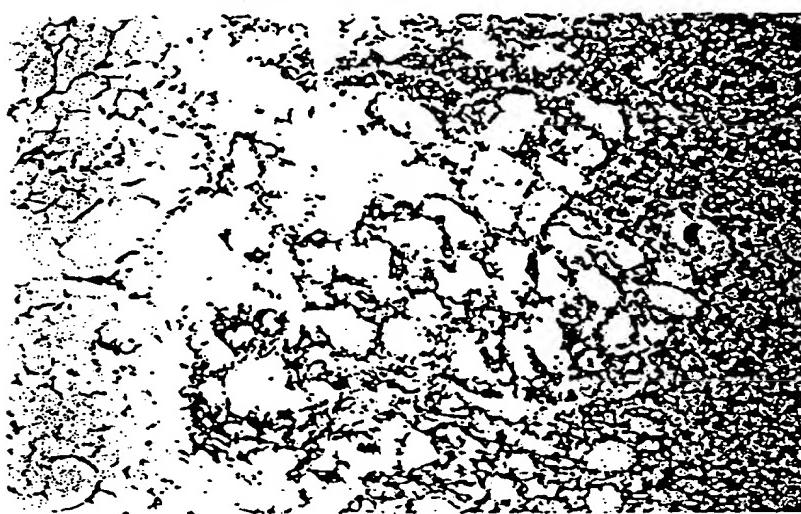
darkfield

FIGURE II B



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lightfield



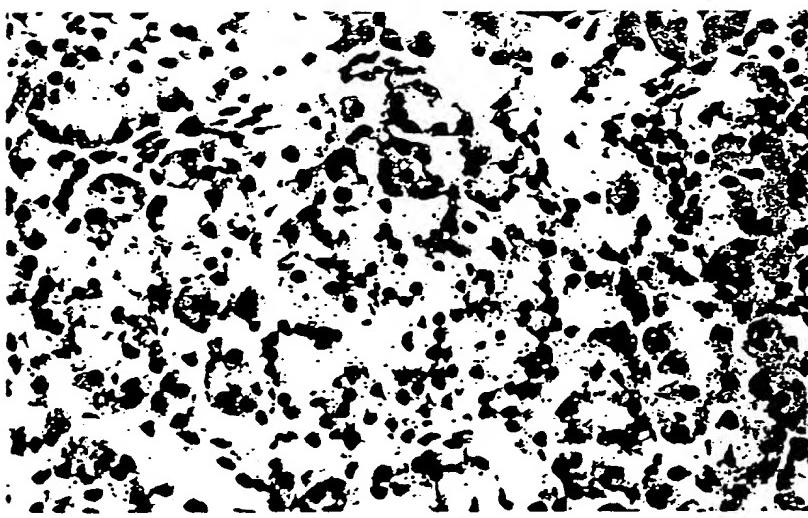
darkfield

FIGURE 12B



FIGURE 13A

lightfield



darkfield

FIGURE 13B

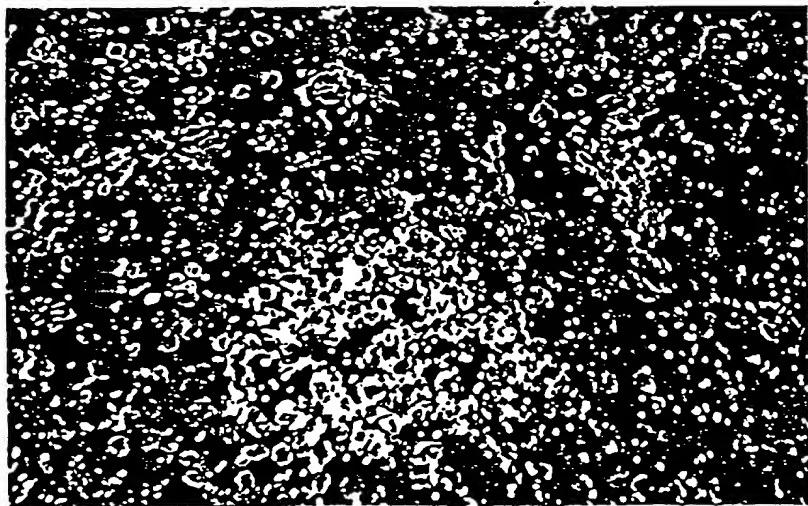
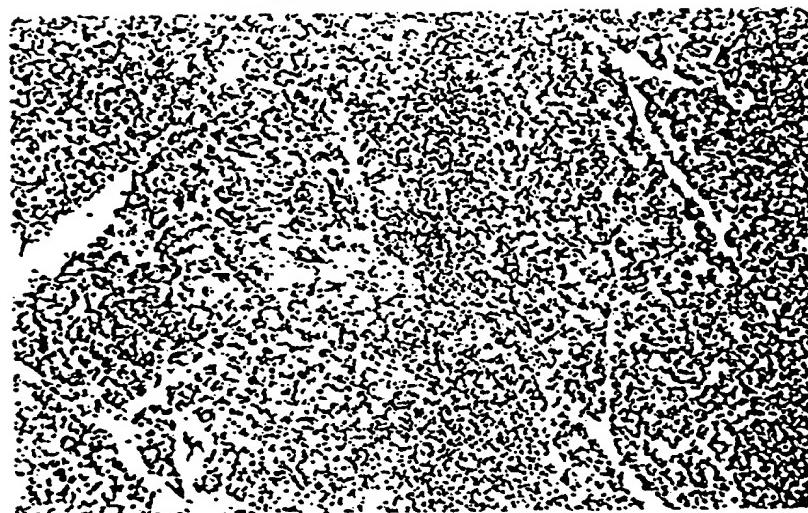


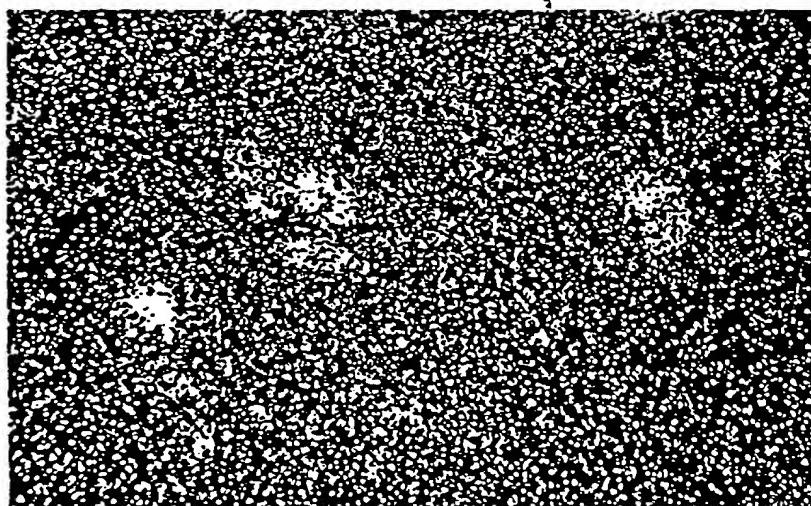
FIGURE 14A

lightfield



darkfield

FIGURE 14B

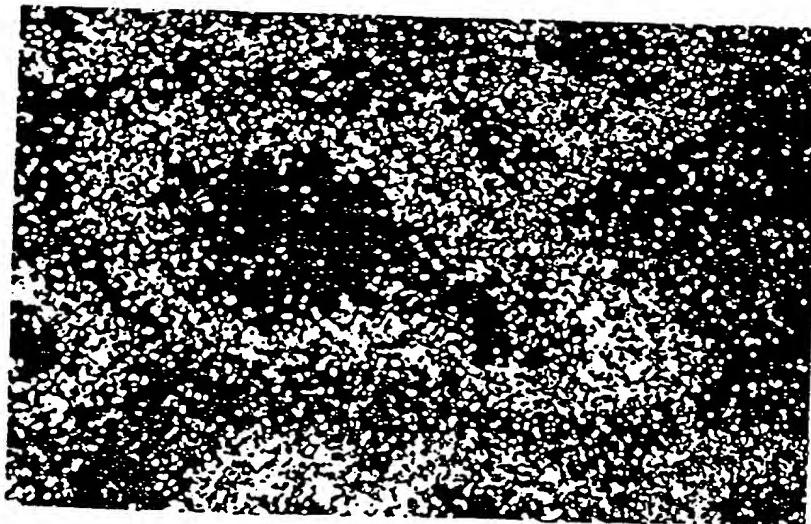


lightfield



darkfield

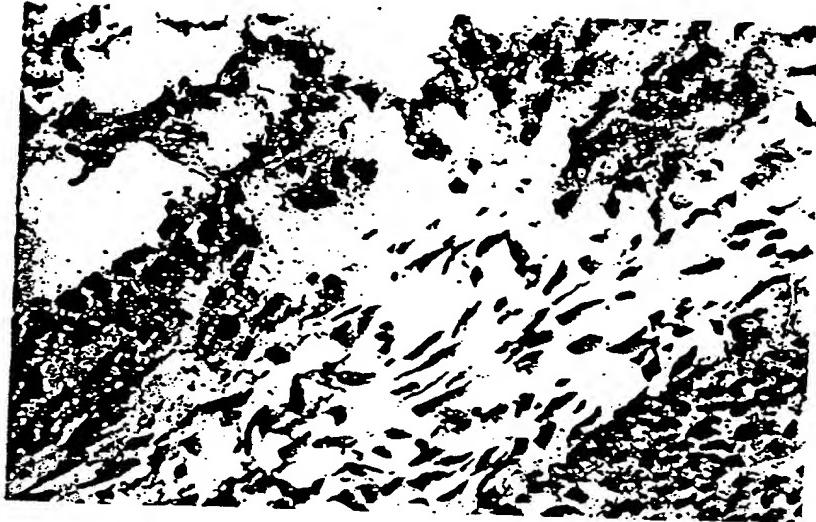
FIGURE 15B



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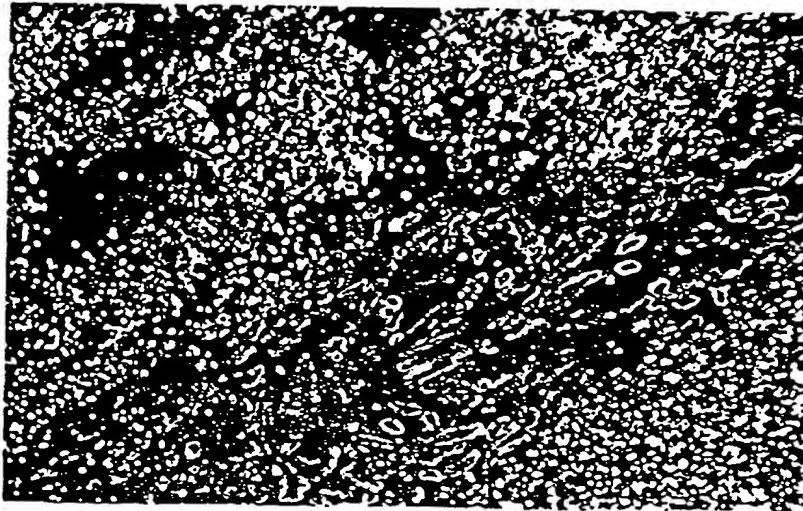
FIGURE 16A

lightfield



darkfield

FIGURE 16B

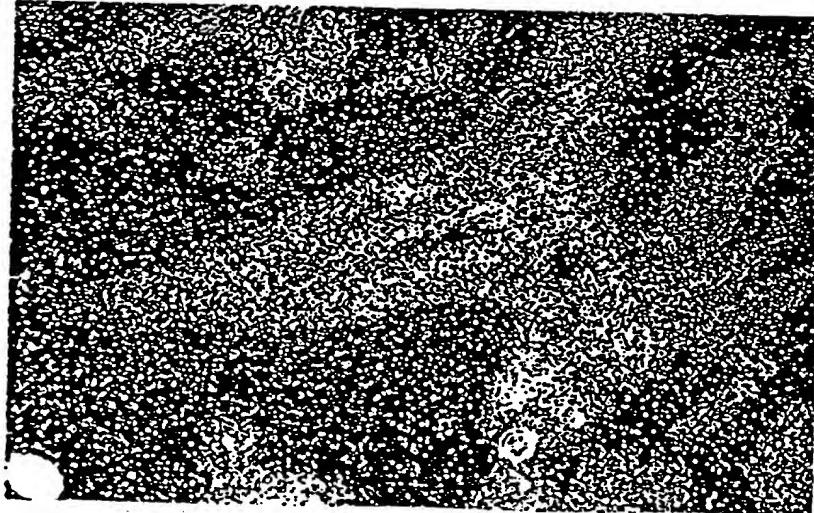


lightfield

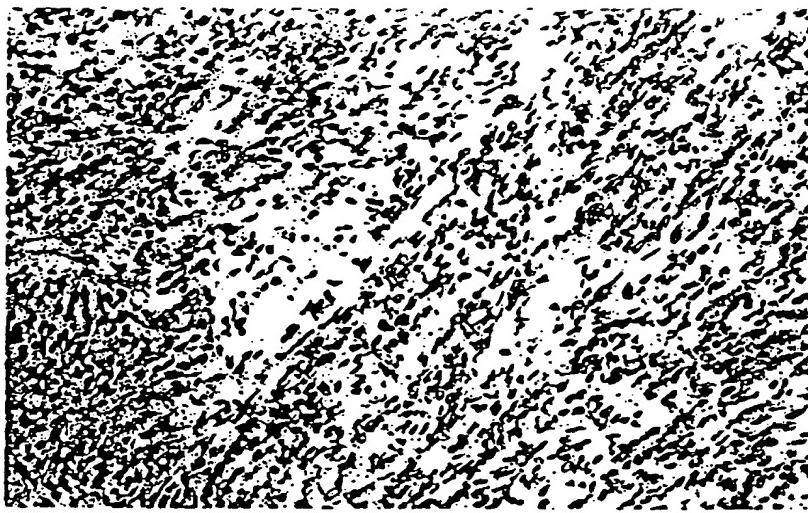


darkfield

FIGURE 17B



lightfield



darkfield

FIGURE 18B

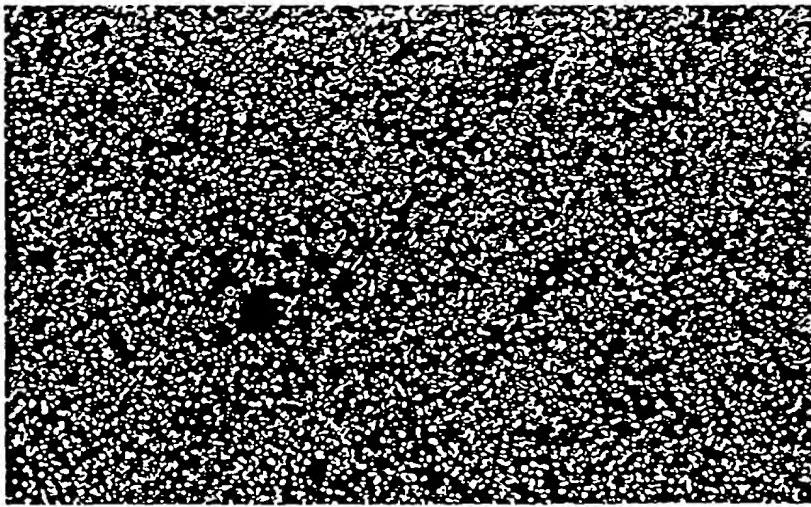
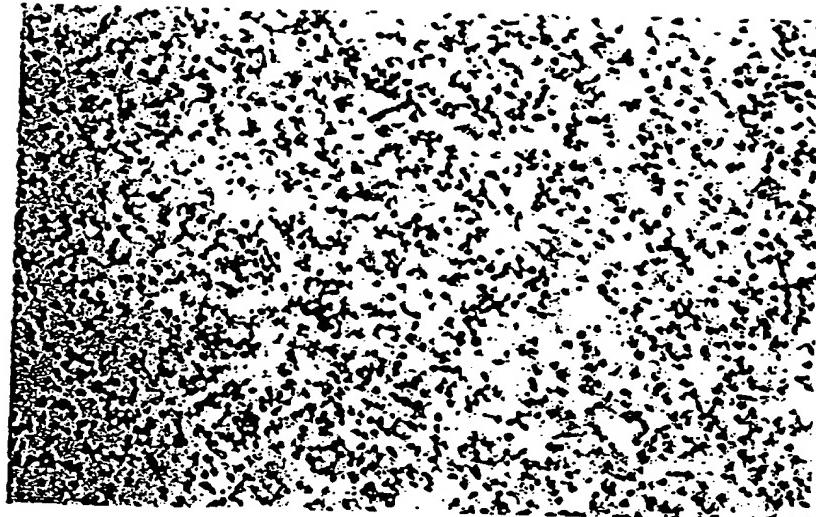


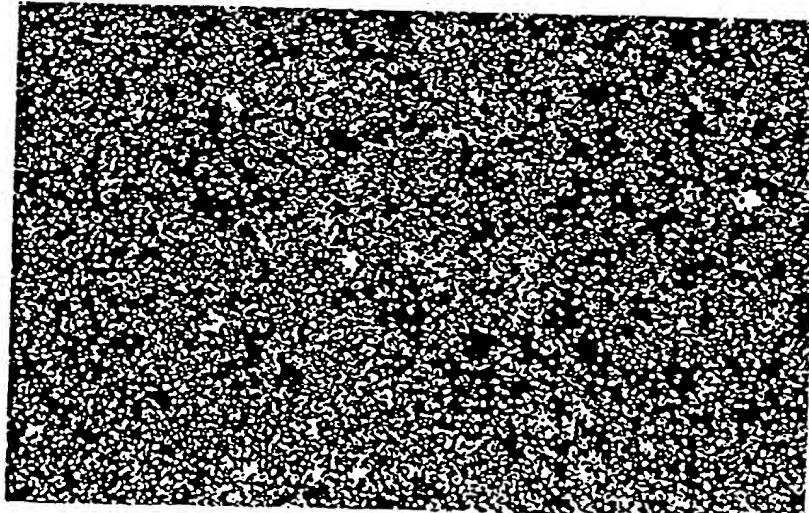
FIGURE 19A

lightfield



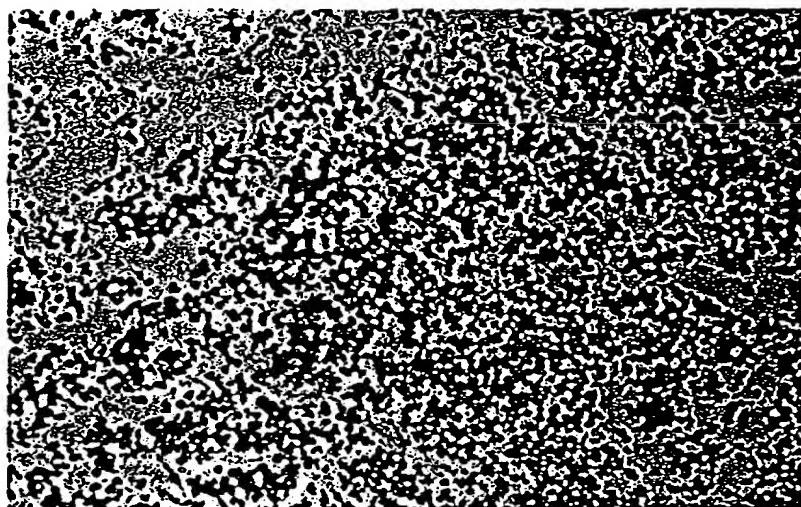
darkfield

FIGURE 19B

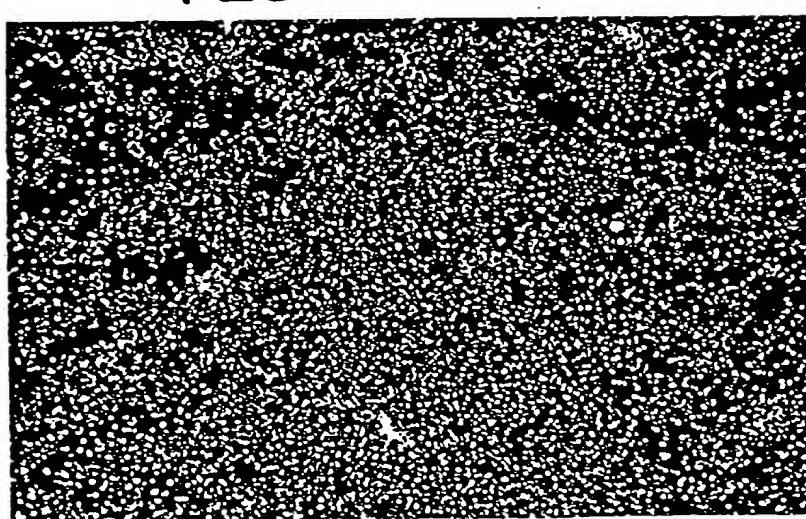


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lightfield



darkfield



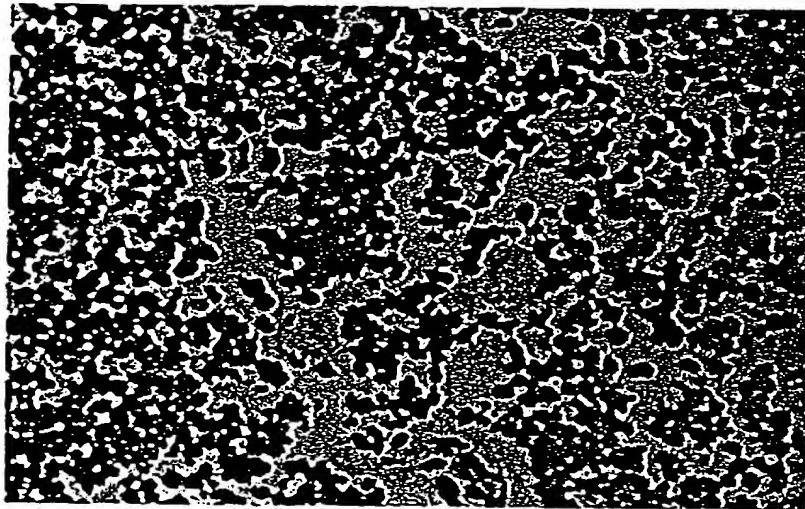
00000000000000000000000000000000

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FIGURE 21A

lightfield



darkfield

FIGURE 21B

